

SEQUENCE LISTING



<110> Fritig, Bernard
Toquin, Valerie
Geoffroy, Pierrette
Legrand, Michel
Kauffmann, Serge

<120> INDUCIBLE COMTII PROMOTER, CHIMERA GENE
CONTAINING SAME AND TRANSFORMED PLANTS

<130> A34638-PCT-USA

<140> US 09/937,204

<141> 2000-03-22

<150> PCT/FR99/03700

<151> 1999-03-22

<150> PCT/FR99/07646

<151> 1999-06-11

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1863

<212> DNA

<213> Nicotiana tabacum

<220>

<221> misc_signal

<222> (667)...(672)

<223> Inverted W box

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<222> (820)...(830)

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<222> (1034)...(1047)

<223> P box

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<222> (1221)...(1226)

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<222> (1343)...(1356)

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 <222> (1369)...(1374)
 <223> A box

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 <222> (1681)...(1690)
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 <222> (1695)...(1699)

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 <222> (1772)...(0)
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 agaaattgaa aaaagaaata ttctatttca ctattatggt aggtgcaact atatcatcac 180
 catggaaaag ccggagtaaa aagagaacgt agaggagatt tcatgatttg attgagaata 240
 taatatatta tttttttgta attccacaca aagattaaga aaatgatctg atcaatgatg 300
 gctccgagga tttggctgtc gcgggaacta tgacattaat ataaatttgt cgctgcctat 360
 aaagacccta tctatctatc tatctatcta tatatatata tatatatata tatatatata 420
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<212> DNA

<213> Nicotiana tabacum

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<222> (1772)...(0)

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<222> (3945)...(4726)

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taatataatta	tttttttgta	attccacaca	aagattaaga	aaatgatctg	atcaatgatg	300
gctccgagga	tttggtgtgc	gcgggaacta	tgacattaat	ataaatttgt	cgctgcctat	360
aaagacccta	tctatctatc	tatctatcta	tatatatata	tatatatata	tatatatata	420
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ataatttctt	ctttttcttg	ttttcacatt	agaaatcaaa	ataaaacaca	agctttttgt	780
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aagcaaatcc	gcacttgata	agtggctaag	tccactttct	agtggaccta	gtggttcact	960
aactttttacc	aaaaaggcaa	taattttgcaa	ttcaaaaaga	aaaaaggaaa	aaagaaaact	1020
agacagactt	taacacacca	actcccacag	gaagcaacaa	tgcaactcac	aaaaggaaaac	1080
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<210> 3

<211> 1095

<212> DNA

<213> *Nicotiana tabacum*

<220>

<221> CDS

<222> (1)...(1095)

<400> 3

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cgt aac tgc aca tat gcc atg caa cta ttg tca tct tca gtc ctc ccc 96
Arg Asn Cys Thr Tyr Ala Met Gln Leu Leu Ser Ser Ser Val Leu Pro
20 25 30

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ttt gtg ttg cat tca aca att caa ttg gaa gtt ttt gag ata tta gcc 144
Phe Val Leu His Ser Thr Ile Gln Leu Glu Val Phe Glu Ile Leu Ala
35 40 45

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aaa tct aat gac act aaa ctt tct gct tct caa att gtt tct caa att 192
Lys Ser Asn Asp Thr Lys Leu Ser Ala Ser Gln Ile Val Ser Gln Ile
50 55 60

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cct aac tgc aca aaa cct gaa gca cct act atg tta aat agg atg ctt 240
Pro Asn Cys Thr Lys Pro Glu Ala Pro Thr Met Leu Asn Arg Met Leu
65 70 75 80

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tat gtc ttg gct agt tac tcc ttg ttt act tgt tcc att gtt gaa gat 288
Tyr Val Leu Ala Ser Tyr Ser Leu Phe Thr Cys Ser Ile Val Glu Asp
85 90 95

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gaa aaa aat aat ggg ggc caa aaa aga gtg tat ggt ttg tca caa gtg 336
Glu Lys Asn Asn Gly Gly Gln Lys Arg Val Tyr Gly Leu Ser Gln Val
100 105 110

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gga aaa ttc ttt gtt aaa aat gaa aat ggt gca tca atg ggg cca ctt 384
Gly Lys Phe Phe Val Lys Asn Glu Asn Gly Ala Ser Met Gly Pro Leu
115 120 125

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ttg gct ttg ctt caa aat aaa gta ttc ata aac agc tgg ttt gaa cta 432

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Lys	Asp	Ala	Val	Leu	Glu	Gly	Gly	Val	Pro	Phe	Asp	Arg	Val	His	Gly	
145					150					155					160	
gtg	cat	gca	ttt	gaa	tat	cca	aaa	tcg	gac	cca	aaa	ttc	aat	gat	ggt	528
Val	His	Ala	Phe	Glu	Tyr	Pro	Lys	Ser	Asp	Pro	Lys	Phe	Asn	Asp	Val	
				165					170					175		
ttc	aac	aag	gca	atg	atc	aat	cac	aca	act	gta	gtc	atg	aaa	aaa	ata	576
Phe	Asn	Lys	Ala	Met	Ile	Asn	His	Thr	Thr	Val	Val	Met	Lys	Lys	Ile	
			180					185					190			
ctt	gaa	aat	tac	aaa	ggt	ttt	gag	aac	ctt	aaa	act	ttg	ggt	gat	ggt	624
Leu	Glu	Asn	Tyr	Lys	Gly	Phe	Glu	Asn	Leu	Lys	Thr	Leu	Val	Asp	Val	
		195					200					205				
gga	ggt	ggt	ctt	gga	ggt	aac	ctc	aag	atg	att	aca	tct	aaa	tac	ccc	672
Gly	Gly	Gly	Leu	Gly	Val	Asn	Leu	Lys	Met	Ile	Thr	Ser	Lys	Tyr	Pro	
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aca	att	aag	ggc	act	aat	ttt	gat	ttg	cca	cat	ggt	ggt	caa	cat	gcc	720
Thr	Ile	Lys	Gly	Thr	Asn	Phe	Asp	Leu	Pro	His	Val	Val	Gln	His	Ala	
225					230					235					240	
cct	tcc	tat	cct	ggg	gtg	gaa	cat	ggt	ggg	gga	gat	atg	ttt	gaa	agt	768
Pro	Ser	Tyr	Pro	Gly	Val	Glu	His	Val	Gly	Gly	Asp	Met	Phe	Glu	Ser	
				245					250					255		
ggt	cca	gaa	gga	gat	gct	att	ttt	atg	aag	tgg	att	ctt	cat	gac	tgg	816
Val	Pro	Glu	Gly	Asp	Ala	Ile	Phe	Met	Lys	Trp	Ile	Leu	His	Asp	Trp	
			260					265					270			
agt	gat	agt	cac	aac	ctc	aag	ttg	cta	aag	aac	tgc	tac	aag	gct	cta	864
Ser	Asp	Ser	His	Asn	Leu	Lys	Leu	Leu	Lys	Asn	Cys	Tyr	Lys	Ala	Leu	
		275					280					285				
cca	gac	aat	gga	aag	gtg	att	ggt	ggt	gag	gcc	att	tta	cca	gtg	aaa	912
Pro	Asp	Asn	Gly	Lys	Val	Ile	Val	Val	Glu	Ala	Ile	Leu	Pro	Val	Lys	
	290					295					300					
cca	gac	att	gac	acc	gca	gtg	ggt	ggc	ggt	tcg	caa	tgt	gat	ttg	atc	960
Pro	Asp	Ile	Asp	Thr	Ala	Val	Val	Gly	Val	Ser	Gln	Cys	Asp	Leu	Ile	
305					310					315					320	
atg	atg	gct	caa	aat	cct	gga	ggc	aaa	gag	cga	tcg	gaa	gag	gag	ttt	1008
Met	Met	Ala	Gln	Asn	Pro	Gly	Gly	Lys	Glu	Arg	Ser	Glu	Glu	Glu	Phe	
				325					330					335		
cga	gcc	ttg	gct	act	gaa	gct	gga	ttc	aaa	ggc	ggt	aac	tta	ata	tgt	1056
Arg	Ala	Leu	Ala	Thr	Glu	Ala	Gly	Phe	Lys	Gly	Val	Asn	Leu	Ile	Cys	
			340					345					350			
tgt	gtc	tgt	aat	ttt	tgg	gtc	atg	gaa	ttc	tgc	aag	tag				1095
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355

360

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<210> 6
<211> 25
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 <213> Phytophthora megasperma

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 Ser Ala Asn Ala Thr Ala Cys Thr Ala Thr Gln Gln Thr Ala Ala Tyr
 20 25 30

 aag aca ctc gtg agc atc ctg tcg gac gcg tcg ttc aac aag tgc tct 144

Lys	Thr	Leu	Val	Ser	Ile	Leu	Ser	Asp	Ala	Ser	Phe	Asn	Lys	Cys	Ser	
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Thr	Asp	Ser	Gly	Tyr	Ser	Met	Leu	Thr	Ala	Lys	Ala	Leu	Pro	Thr	Thr	
	50					55				60						
gcg	cag	tac	aag	ctc	atg	tgc	gcg	tcc	acg	gca	tgc	aac	acc	atg	atc	240
Ala	Gln	Tyr	Lys	Leu	Met	Cys	Ala	Ser	Thr	Ala	Cys	Asn	Thr	Met	Ile	
	65				70				75						80	
aag	aag	atc	gtg	acg	ctg	aac	ccg	ccc	aac	tgc	gac	ctg	acg	gtg	ccc	288
Lys	Lys	Ile	Val	Thr	Leu	Asn	Pro	Pro	Asn	Cys	Asp	Leu	Thr	Val	Pro	
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acg	agc	ggc	ctg	gtg	ctc	aac	gtg	tac	tcg	tac	gcg	aac	ggc	ttc	tcg	336
Thr	Ser	Gly	Leu	Val	Leu	Asn	Val	Tyr	Ser	Tyr	Ala	Asn	Gly	Phe	Ser	
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Asp	Lys	Cys	Ser	Ser	Leu											
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 <222> (1)...(294)

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1				5				10						15		
agc	atc	ctg	tcg	gac	gcg	tcg	ttc	aac	aag	tgc	tct	acg	gat	tcg	ggc	96
Ser	Ile	Leu	Ser	Asp	Ala	Ser	Phe	Asn	Lys	Cys	Ser	Thr	Asp	Ser	Gly	
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tac	tcc	atg	ctg	acg	gcc	aag	gcc	ctc	ccc	acc	acg	gcg	cag	tac	aag	144
Tyr	Ser	Met	Leu	Thr	Ala	Lys	Ala	Leu	Pro	Thr	Thr	Ala	Gln	Tyr	Lys	
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ctc	atg	tgc	gcg	tcc	acg	gca	tgc	aac	acc	atg	atc	aag	aag	atc	gtg	192
Leu	Met	Cys	Ala	Ser	Thr	Ala	Cys	Asn	Thr	Met	Ile	Lys	Lys	Ile	Val	
	50					55				60						
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Thr	Leu	Asn	Pro	Pro	Asn	Cys	Asp	Leu	Thr	Val	Pro	Thr	Ser	Gly	Leu	
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gtg	ctc	aac	gtg	tac	tcg	tac	gcg	aac	ggc	ttc	tcg	gac	aag	tgc	tcg	288
Val	Leu	Asn	Val	Tyr	Ser	Tyr	Ala	Asn	Gly	Phe	Ser	Asp	Lys	Cys	Ser	
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tcg ctg
Ser Leu

294

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<221> CDS
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<223> CDS megaspermine

<223> Synthetic construct

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gtacatgatt gtgaagccta acaaaaacac tctaaaaggc ctctagagga tccccggggt 1260
acc atg aac ttc acc gct ctg ctc gct gcc gtc gcc gcc gcc ttg gtc 1308
Met Asn Phe Thr Ala Leu Leu Ala Ala Val Ala Ala Ala Leu Val
1 5 10 15

gga tct gcc aac gcc acc gcg tgc acc gcc acc cag caa acc gct gcg 1356
Gly Ser Ala Asn Ala Thr Ala Cys Thr Ala Thr Gln Gln Thr Ala Ala
20 25 30

tac aaa aca ctc gtg agc atc ctg tcg gac gcg tcg ttc aac aag tgc 1404
Tyr Lys Thr Leu Val Ser Ile Leu Ser Asp Ala Ser Phe Asn Lys Cys
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acg	gcg	cag	tac	aag	ctc	atg	tgc	gcg	tcc	acg	gca	tgc	aac	acc	atg	1500
Thr	Ala	Gln	Tyr	Lys	Leu	Met	Cys	Ala	Ser	Thr	Ala	Cys	Asn	Thr	Met	
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atc	aaa	aaa	atc	gtg	acg	ctg	aac	ccg	ccc	aac	tgc	aac	ctg	acg	gtg	1548
Ile	Lys	Lys	Ile	Val	Thr	Leu	Asn	Pro	Pro	Asn	Cys	Asn	Leu	Thr	Val	
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ccc	acg	agc	ggc	ctg	gtg	ctc	aac	gtg	tac	tcg	tac	cca	aac	ggc	ttc	1596
Pro	Thr	Ser	Gly	Leu	Val	Leu	Asn	Val	Tyr	Ser	Tyr	Pro	Asn	Gly	Phe	
			100					105					110			
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